

FIG. 1

Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3.5	0.121	0.036	0.467	0.664
4	0.096	0.06	0.519	0.708
4.5	0.078	0.079	0.565	0.745
5	0.062	0.098	0.615	0.782
5.5	0.05	0.127	0.659	0.813
6	0.04	0.163	0.694	0.836
6.5	0.033	0.202	0.725	0.855
7	0.025	0.248	0.763	0.878
7.5	0.021	0.304	0.78	0.889
8	0.015	0.368	0.816	0.909
8.5	0.012	0.418	0.836	0.92
9	0.009	0.512	0.856	0.93
9.5	0.007	0.581	0.863	0.934
10	0.006	0.679	0.835	0.919

FIG. 2

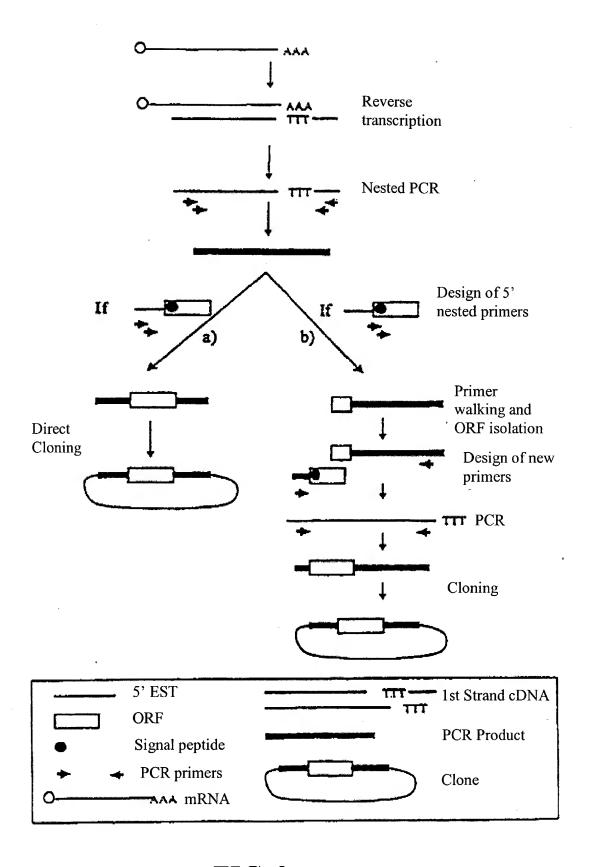
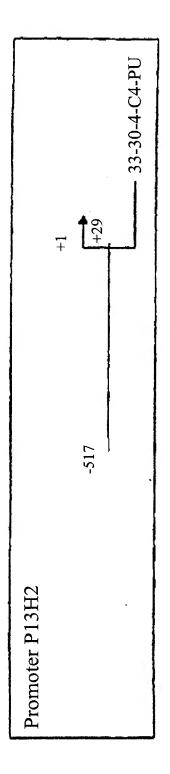
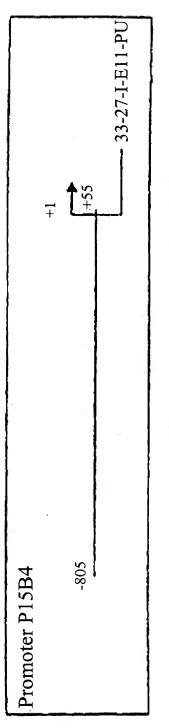


FIG. 3

Description of promoters structure isolated from SignalTag 5' ESTs





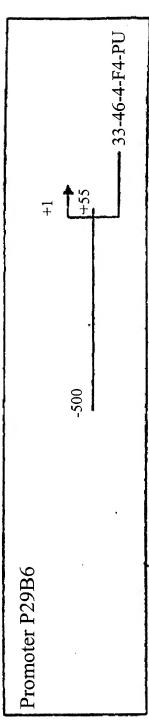


FIG. 4

Description of Transcription Factor Binding Sites present on promoters isolated from SignalTag sequences

Promoter coguence D1	2U2 /546 L-					
Promoter sequence P1					•	2
Matrix	Position	Orientation	Score	Length	Sequence	Location in:
						SEQ ID NO: 17
CMYB_01	-502	. +	0.983	9	TGTCAGTTG	17-25
MYOD_Q6	-501	-	0.961	10	CCCAACTGAC	complement of 18-27
S8_01	-444	•	0.960	11	AATAGAATTAG	complement of 75-85
S8 ⁻ 01	-425	+	0.966	11	AACTAAATTAG	94-104
DELTAEFI 01	-390	•	0 960	11	GCACACCTCAG	complement of 129-139
GATA C	-364		0.964	11	AGATAAATCCA	complement of 155-165
CMYB 01	-349	+	0.958	9	CTTCAGTTG	170-178
GATAI 02	-343	+	0.959	14	TTGTAGATAGGACA	176-189
GATA_C	-339	+	0.953	11	AGATAGGACAT	180-190
TALIALPHAE47 01	-235	+ -	0.973	16	CATAACAGATGGTAAG	
TALIBETAE47 01	-235	+		16		284-299
	-235 -235	+ +	0.983		CATAACAGATGGTAAG	284-299
TALIBETAITF2_01			0.978	16	CATAACAGATGGTAAG	284-299
MYOD_Q6	-232	•	0.954	10	ACCATCTGTT	complement of 287-296
GATA1_04	-217	-	0.953	13	TCAAGATAAAGTA	complement of 302-314
IK1_01	-126	+	0.963	13	AGTTGGGAATTCC	393-405
IK2_01	-126	+	0.985	12	AGTTGGGAATTC	393-404
CREL_01	-123	+	0.962	10	TGGGAATTCC	396-405
GATA1_02	-96	+	0.950	14	TCAGTGATATGGCA	423-436
SRY 02	-41	-	0.951	12	TAAAACAAAACA	complement of 478-489
E2F 02	-33	+	0.957	8	TTTAGCGC	486-493
MZF1_01	-5	-	0.975	8	TGAGGGA	complement of \$14-521
			0.2.0	-		complement of 514-521
Promoter sequence P1	5B4 (861 bn):				_
Matrix	Position	Orientation	Score	Length	Sequence	Location in:
		J. 10	0.0.0	~-c	3342323	SEQ ID NO: 20
NFY_Q6	-748	•	0.956	11	GGACCAATCAT	complement of 60-70
MZFĪ 01	-738	+	0.962	8	CCTGGGGA	70-77
CMYB 01	-684	+	0.994	ğ	TGACCGTTG	124-132
		•	U.77 7		10ACCG1 (G	124-132
VMVR 02	692		0.095	0	TCCAACGGT	
VMYB_02	-682	-	0.985	9	TCCAACGGT	complement of 126-134
STAT_01	-673	+	0.968	9	TTCCTGGAA	135-143
STAT_01 STAT_01	-673 -673	+ -	0.968 0.951	9 9	TTCCTGGAA TTCCAGGAA	135-143 complement of 135-143
STAT_01 STAT_01 MZF1_01	-673 -673 -556	+ - -	0.968 0.951 0.956	9 9 8	TTCCTGGAA TTCCAGGAA TTGGGGGA	135-143 complement of 135-143 complement of 252-259
STAT_01 STAT_01 MZF1_01 IK2_01	-673 -673 -556 -451	+ - - +	0.968 0.951 0.956 0.965	9 9 8 12	TTCCTGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC	135-143 complement of 135-143 complement of 252-259 357-368
STAT_01 STAT_01 MZF1_01 IK2_0I MZF1_01	-673 -673 -556 -451 -424	+ - -	0.968 0.951 0.956 0.965 0.986	9 9 8 12 8	TTCCTGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA	135-143 complement of 135-143 complement of 252-259 357-368 384-391
STAT_01 STAT_01 MZF1_01 IK2_0I MZF1_01 SRY_02	-673 -673 -556 -451 -424 -398	+ - • + -	0.968 0.951 0.956 0.965 0.986 0.955	9 9 8 12 8 12	TTCCTGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421
STAT 01 STAT 01 MZF1 01 IK2 0I MZF1 01 SRY 02 MZF1 01	-673 -673 -556 -451 -424 -398 -216	+ - - + +	0.968 0.951 0.956 0.965 0.986	9 8 12 8 12 8	TTCCTGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA	135-143 complement of 135-143 complement of 252-259 357-368 384-391
STAT_01 STAT_01 MZF1_01 IK2_0I MZF1_01 SRY_02 MZF1_01 MYOD_Q6	-673 -673 -556 -451 -424 -398 -216 -190	+ - • + -	0.968 0.951 0.956 0.965 0.986 0.955	9 9 8 12 8	TTCCTGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01	-673 -673 -556 -451 -424 -398 -216	+ - - + - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960	9 8 12 8 12 8	TTCCTGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01	-673 -673 -556 -451 -424 -398 -216 -190	+ - - + - - +	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981	9 8 12 8 12 8	TTCCTGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01	-673 -673 -556 -451 -424 -398 -216 -190 -176	+ - + + - +	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958	9 9 8 12 8 12 8 10	TTCCTGGAA TTCCAGGAA TTGGGGGA GAATGGGGATTTC AGAGGGGA GAAACAAAACA	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01	-673 -673 -556 -451 -424 -398 -216 -190 -176	+ - + + - +	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992	9 9 8 12 8 12 8 10 11	TTCCTGGAA TTCCAGGAA TTCGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01	-673 -673 -556 -451 -424 -398 -216 -190 -176 5	+ - + + - + + -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992	9 9 8 12 8 12 8 10 11	TTCCTGGAA TTCCAGGAA TTCGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01	-673 -673 -556 -451 -424 -398 -216 -190 -176 5	+ - + + - + + -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992	9 9 8 12 8 12 8 10 11	TTCCTGGAA TTCCAGGAA TTCGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16	+ - - + + - + - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986	9 9 8 12 8 10 11 11 8	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16	+ - - + + - + - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986	9 9 8 12 8 10 11 11 8	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position	+ - - + - + + - - - Orientation	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986	9 9 8 12 8 10 11 11 8 Length	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_06 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position	+ - - + - + + - - Orientation + +	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986 Score	9 9 8 12 8 10 11 11 8 Leugth	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309	+ + + + + + + - - Orientation + + +	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986 Score	9 9 8 12 8 10 11 11 8 Length	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAAAAACA GAAGGGGA AGCATCTGCC TCCCACCTTCC GAGGCAATTAT AGAGGGGA Sequence GGACTCACGTGCTGCT ACTCACGTGCTG ACTCACGTGCTG	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309	+ - - + + + - - Orientation + + +	0.968 0.951 0.956 0.965 0.986 0.955 0.980 0.981 0.958 0.992 0.986 Score 0.964 0.965 0.985	9 9 8 12 8 10 11 11 8 Length	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAAAAAAA GAAGGGA AGCATCTGCC TCCCACCTTCC GAGGCAATTAT AGAGGGGA Sequence GGACTCACGTGCTGCT ACTCACGTGCTG ACTCACGTGCTG CAGCACGTGAGT	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 193-204 complement of 193-204
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01 NMYC_01	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309 -309	+ + + + + + + - - Orientation + + +	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986 Score 0.964 0.965 0.985 0.985	9 9 8 12 8 10 11 11 8 Length 16 12 12 12	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 193-204 complement of 193-204 complement of 193-204
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309 -309 -309	+ + + + + + + - - Orientation + + + -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986 Score 0.964 0.965 0.985 0.985 0.995	9 9 8 12 8 10 11 11 8 Length 16 12 12 12 12	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 193-204 complement of 193-204 complement of 193-204 complement of 193-204
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02 USF_C	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309 -309 -309 -309	+ + + + + + + - - Orientation + + + - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.988 0.992 0.986 Score 0.964 0.965 0.985 0.985 0.995 0.995	9 9 8 12 8 10 11 11 8 Length 16 12 12 12 12 12 8	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 193-204 complement of 193-204 complement of 193-204 complement of 193-204
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02 USF_C USF_C	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309 -309 -309 -307 -307	+ + + + + + - - Orientation + + + - - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.988 0.992 0.986 Score 0.964 0.965 0.985 0.985 0.985 0.992	9 9 8 12 8 10 11 11 8 Length 16 12 12 12 12 12 12 8 8	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 complement of 193-204
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01 NMYC_01 MYCMAX_02 USF_C USF_C MZF1_01	-673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309 -309 -309 -307 -307	+ + + + + + + - - Orientation + + + - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986 Score 0.964 0.965 0.985 0.985 0.985 0.997 0.997	9 9 8 12 8 10 11 11 8 Length 16 12 12 12 12 12 12	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 complement of 193-202 complement of 195-202 complement of 210-217
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_06 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01 NMYC_01 USF_01 MYCMAX_02 USF_C USF_C MZF1_01 ELK1_02	-673 -673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309 -309 -309 -307 -307 -292 -105	+ + + + + + + - - Orientation + + + - - - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986 0.965 0.985 0.985 0.985 0.972 0.997 0.991 0.968 0.963	9 9 8 12 8 10 11 11 8 Length 16 12 12 12 12 12	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 193-204 complement of 193-204 195-202 complement of 195-202 complement of 210-217 397-410
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_06 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01 USF_01 NMYC_MAX_02 USF_C USF_C MZF1_01 ELK1_02 CETSIP54_01	-673 -673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309 -309 -309 -309 -307 -307 -292 -105 -102	+ + + + + + + - - Orientation + + + - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986 0.985 0.985 0.985 0.985 0.997 0.997 0.997	9 9 8 12 8 10 11 11 8 Length 16 12 12 12 12 12 12 12	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAAAAAAA GAAGGGA AGCATCTGCC TCCCACCTTCC GAGGCAATTAT AGAGGGA Sequence GGACTCACGTGCTGCT ACTCACGTGCTG ACTCACGTGCTG CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC GCACGTGA CTCACGTGC GCACGTGA CTCACGTGC CTCCCGGAAGCCT TCCCGGAAGCC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 193-204 complement of 193-204 195-202 complement of 195-202 complement of 210-217 397-410 400-409
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01 USF_01 NMYC_MAX_02 USF_C USF_C USF_C MZF1_01 ELK1_02 CETS1P54_01 AP1_Q4	-673 -673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309 -309 -309 -307 -307 -292 -105 -102 -42	+ + + + + + + - - Orientation + + + - - - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986 0.965 0.985 0.985 0.985 0.972 0.997 0.991 0.968 0.963	9 9 8 12 8 10 11 11 8 Length 16 12 12 12 12 12 12 11 11	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAAAAACA GAAGGGGA AGCATCTGCC TCCCACCTTCC GAGGCAATTAT AGAGGGGA Sequence GGACTCACGTGCTGCT ACTCACGTGCTG ACTCACGTGCTG CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC GCACGTGA CATGGGGA CTCTCCGGAAGCCT TCCGGAAGCC AGTGACTGAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 complement of 195-202 complement of 210-217 397-410 400-409 complement of 460-470
STAT_01 STAT_01 MZF1_01 IK2_0I MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01 NMYC_01 USF_01 NMYC_01 MYCMAX_02 USF_C USF_C MZF1_01 ELK1_02 CETSIP54_01 AP1_Q4 AP1F1_Q2	-673 -673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309 -309 -309 -307 -307 -292 -105 -102 -42	+ + + + + + + - - Orientation + + + - - - - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986 0.985 0.985 0.985 0.985 0.997 0.997 0.997	9 9 8 12 8 10 11 11 8 Length 16 12 12 12 12 12 12 11 11 11	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAACAAAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 complement of 195-202 complement of 210-217 397-410 400-409 complement of 460-470 complement of 460-470
STAT_01 STAT_01 MZF1_01 IK2_01 MZF1_01 SRY_02 MZF1_01 MYOD_Q6 DELTAEF1_01 S8_01 MZF1_01 Promoter sequence P2 Matrix ARNT_01 NMYC_01 USF_01 USF_01 USF_01 NMYC_MAX_02 USF_C USF_C USF_C MZF1_01 ELK1_02 CETS1P54_01 AP1_Q4	-673 -673 -673 -556 -451 -424 -398 -216 -190 -176 5 16 9B6 (555 bp Position -311 -309 -309 -309 -309 -309 -307 -307 -292 -105 -102 -42	+ + + + + + + - - Orientation + + + - - - - -	0.968 0.951 0.956 0.965 0.986 0.955 0.960 0.981 0.958 0.992 0.986 0.985 0.985 0.985 0.985 0.997 0.997 0.997 0.991 0.968 0.963 0.974 0.963	9 9 8 12 8 10 11 11 8 Length 16 12 12 12 12 12 12 11 11	TTCCTGGAA TTCCAGGAA TTCCAGGAA TTCCAGGAA TTGGGGGA GAATGGGATTTC AGAGGGGA GAAAAAAACA GAAGGGGA AGCATCTGCC TCCCACCTTCC GAGGCAATTAT AGAGGGGA Sequence GGACTCACGTGCTGCT ACTCACGTGCTG ACTCACGTGCTG CAGCACGTGAGT CAGCACGTGAGT CAGCACGTGAGT TCACGTGC GCACGTGA CATGGGGA CTCTCCGGAAGCCT TCCGGAAGCC AGTGACTGAAC	135-143 complement of 135-143 complement of 252-259 357-368 384-391 complement of 410-421 592-599 618-627 632-642 complement of 813-823 complement of 824-831 Location in: SEQ ID NO: 23 191-206 193-204 complement of 195-202 complement of 210-217 397-410 400-409 complement of 460-470